AMENDMENTS TO THE CLAIMS

This listing replaces all prior versions and listings of claims in the application.

Listing of Claims

1. (Cancelled)

2. (Cancelled)

3. (Withdrawn) An information recording medium in which program information for causing a computer system to carry out the individual procedures making up said biopolymer automatic identifying method according to claim 1 or 2 is stored.

4. (Cancelled)

5. (Currently Amended) The biopolymer automatic identifying method according to claim 9, wherein said calibrating step comprises: (A) calculating a relative error between said mass values and the theoretical mass in (d); (B) estimating a systemic error of said mass values by creating a least square line by plotting the theoretical mass in (d) against said relative error; and (C) subtracting said systemic error from said calibrated mass values, X_c.

6. (Previously Presented) The biopolymer automatic identifying method according to claim 9, wherein said sample comprises more than one biopolymer.

7. (Cancelled)

8. (Previously Presented) The biopolymer automatic identifying method according to claim 9, wherein each mass value is matched with one candidate molecule.

9. (Currently Amended) A biopolymer automatic identifying method, comprising:

(a) ~~inputting into a computer system~~ obtaining a plurality of observed mass values, ~~obtained~~ by subjecting a sample comprised of one or more biopolymers to MS/MS, producing candidate molecules;

(b) matching at least one of said observed mass values with a theoretical mass value, in a predetermined database of known mass values using a suitably programmed

computing device, for ~~at least two~~ candidate molecules, wherein one of said candidate ~~molecule~~ molecules has a high similarity score such that it is thereby identified as an internal reference; then[[,]]

(c) selecting at least one candidate molecule from (b) that has such a high similarity score using a suitably programmed computing device;

(d) calibrating said plurality of observed mass values with said internal reference to produce calibrated mass values using a suitably programmed computing device,

wherein said internal reference is the theoretical mass of the selected candidate molecule or molecules in (c), and

wherein each of said calibrated mass values is determined by the equation

$Xc = X / (1 + (aX + b))$, wherein

Xc is a calibrated mass value,

X is an observed mass value,

$b = \sum\{ (M-mM) X (E-mE) \} / \sum \{ (M-mM)2\}$,

$a = mE - bX\ mM$,

$E = (X-M) /M$,

$mE = \sum (E) /n$, and

$mM = \sum (M) /n$, wherein M is the theoretical mass value for said candidate molecule and n is the total number of candidate molecules;

(e) ~~calculating a relative error and standard deviation of the theoretical mass in (d)~~ calculating relative error between said calibrated mass value of a candidate molecule in (d) and a theoretical mass value to determine the standard deviation of said relative error using a suitably programmed computing device;

(f) determining a tolerance of the matching step using said standard deviation (e) and a suitably programmed computing device, wherein said tolerance is determined by the equation

$T_c = K \times S_{EC}$, wherein K is 1.5 to 3.0; optionally,

(g) repeating steps (b) – (f) using a suitably programmed computing device; and then

(h) comparing said calibrated mass values to said predetermined database, thereby to determine the identity of at least one of said biopolymers using a suitably programmed computing device.

10. (Previously Presented) The biopolymer automatic identifying method according to claim 9, further comprising communicating said identity to a display or to a computer storage medium.